

10 Recd. 09 DEC 2002

## SEQUENCE LISTING

<110> IZUI, MASAKO  
SUGIMOTO, MASAKAZU  
KURAHASHI, OSAMU  
NAKAMATSU, TSUYOSHI

<120> DNA ENCODING SUCROSE PTS ENZYME II

<130> 217677US0PCT

<140> US 10/019,284

<141> 2002-01-02

<150> JP 11-189512

<151> 1999-07-02

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 5969

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (3779)..(5761)

<223>

<400> 1  
agtcgctcga cgccaccatt gatgtggtgg tcaccgagct tgcggaggct ttctacatct 60  
acgctcccggt cggcggtggag tgggggtcatt acgggtggga tcacgccggt gaaagttgctg 120  
gaacccatgg tgttccttgt ggggttgagg aacgagtgcg ggtgagaagt ttttcaagt 180  
tctgcagttt ttaagttatg catcatcagc ttggaaggct gaggtaattc agtagacctg 240  
caacagcagg cctcaagtcc gaagataatt aacctagatc cgtagacata agacatcata 300  
cgctctatgc ttgctggaag gaaccaaata acctcagaaa gatggcagaa gtggtgcatt 360  
atcaagaaaa tgcaggtcaa gcagttaaaa aaattgaggg aagaattgtt cccccctcg 420  
gggtgattga tggttttctc caactcgaaa acggcatcat cacggaactc tctggagaac 480  
cagcacctaa aaacgcagga ttccaccccg aactccccac gattgttccc ggttttattg 540  
atcttcataa tcacggtgga aacggtggcg cgtttcctac gggaaacgcag gaccaggcga 600  
ggaacaccgc gcagtatcac cgccaacatg gcacgaccgt gatgttgcca agcatggttt 660  
cggcgccggc tgacgcactg gcagcgcagg tggaaaacct tattcccttg tgtgaagagg 720  
tctgtctgtg cggcattcac ctgcagggcc ctttcatcaa cgcattgccgt tgtggtgctc 780

aaaaccgga ttccattttt cccggcaacc caacagatct tgcccgggtg atccatgcgg 840  
 gaaaagggtg gatcaaactg atcacagtag cgccggaaac tgacaatctt tctgagcttc 900  
 tcgatctctg cgcagcgcac cacatcattg cttccttcgg gcacactgat gcagattttg 960  
 ataccactac cagcgcgaatt gccttggtta aagagaaaaa tgtgacggtc acggctacgc 1020  
 atttggtcaa tgcgatgcct ccgctgcac atagggctcc cggcagcgtg ggcgctttgc 1080  
 ttgctgcggc acgtgccggg gacgcatatg ttgagttgat cgccgacggc gtgcatttgg 1140  
 ccgatggaac ggtcgatcta gtcgttcca acaacgcctt ttccatcacg gacgccatgg 1200  
 aagccgccgg aatgccagac ggtgagtaca ttttgggctt ttgaaacgtc accgtcaccg 1260  
 atggagtcgc ccgtctgcgc gatggcggcg ccacgcggc gggcaccagc acactagcga 1320  
 gtcagttcgt gcaccacgtg cgcaggggta tgacgcttat cgacgcgacc ctccacacct 1380  
 caaccgtcgc cgctaaaatt ctcggtcttg gcgatcacga aatcgctaaa tccaaccctg 1440  
 caaattttgt ggtctttgac tcaaacggcc aggtgcaaaa ggtccattta ggtcatcaag 1500  
 tactttaagt acgagtaaaa ctatcctgat tttaaaggag tcccaccatg gaaatcacta 1560  
 tctgcaaaga cgagcaagaa gtcggcaaa gagttgcagt cctaatacga cccttcgcca 1620  
 acaagggtgg aaccttgggg cttgcaacag gatcctcacc actgagtacc taccaagagc 1680  
 tcattcgcgt gtatgaagct ggggaagtgt cattcaagaa ctgcaaggca ttcttggttg 1740  
 atgaatacgt gggactaacc cgtgacgatg aaaacagcta ctttaaaacc attcgcaaag 1800  
 agttcactga ccacatcgac atcgttgatg aagaggctta cagcccagat ggtgcaaacc 1860  
 ctgatccata cgaagcagct gcagagtatg aggcaaagat cgctgcagaa tccgttgaag 1920  
 ttcaaatcct tggcatcggc ggaaacggca catcgctttc attgaaccat catcttctct 1980  
 gtcaggactg acaaagggtc aggcgctgca ccctaaaact gtggaggaca acgctcgatt 2040  
 cttcaacacc atcgaagagg tcccaaccca cgccgtcacc cagggttttg gcactttgtc 2100  
 ccgcgcgcaa aacatcgtgt tgggtggcaac tgggtgaagga aaagccgacg ccacccggc 2160  
 aactgtggaa ggcccagtga ctgcttcttg ccaggttcc atcctgtaga tgcacaacat 2220  
 gccaccatca tcgttggtatg aagcagcagt atccaagctg gaaaacgctg atcactaccg 2280  
 tctcatggag caattaaagc tgcgctagaa acaaaaagga aagtactgtg tggggctatg 2340  
 cacacagaac tttccagttt gcgccctgcg taccatgtga ctctccgca gggcaggctc 2400  
 aatgatccca acggaatgta cgtcgatgga gataccctcc acgtctacta ccagcacgat 2460

ccaggtttcc ccttcgcacc aaagcgcacc ggctgggctc acaccaccac gccgttgacc 2520  
 ggaccgcagc gattgcagtg gacgcacctg cccgacgctc tttaccgga tgcacccat 2580  
 gacctggatg gatgctattc cggtggagcc gtatttactg acggcacact taaacttttc 2640  
 tacaccggca acctaaaaat tgacggaaag cgccgcgcca cccaaaacct tgtcgaagtc 2700  
 gaggacccaa ctgggctgat gggcggcatt catcgccgtt cgcctaaaaa tccgcttata 2760  
 gacggacccg ccagcgggtt cacaccccat taccgcgata ccatgatcag ccctgatggt 2820  
 gatggttgga acatggttct tggggcccaa cgcgaaaacc tcaccggtgc agcggttcta 2880  
 taccgctcga cagatcttga aaactgggaa ttctccggtg aaatcacctt tgacctcagt 2940  
 gatgcacaac ctggttctgc tcctgatctc gttcccgatg gctacatgtg ggaatgcccc 3000  
 aaccttttta cgcttcgcga tgaagaaact ggcgaagatc tcgacgtgct gattttctgt 3060  
 ccacaaggat tggaccgaat ccacgatgag gttactcact acgcaagctc tgaccagtgc 3120  
 ggatatgtcg tcgacaagct tgaaggaacg acctcccgcg tcttgcgagg attcagcgag 3180  
 ctggatttcg gccatgaatt ctacgcaccg caggttgagc taaacggttc tgatgcctgg 3240  
 ctcgtgggct ggatggggct gcccgcgag gatgatcacc caacagttgc acaggaagga 3300  
 tgggtgcact gcctgactgt gccccgcaag cttcatttgc gcaaccacgc gatctaccaa 3360  
 gagctccttc tcccagaggg ggagtcgggg gtaatcagat ctgtattagg ttctgaacct 3420  
 gtccgagtag acatccgagg caatatttcc ctcgagtggg atgggtgccg tttgtctgtg 3480  
 gatcgtgatg gtgatcgtcg cgtagctgag gtaaaacctg gcgaattagt gatcgcgagc 3540  
 gataatacag ccattgagat aactgcaggt gatggacagg ttctattcgc ttttccgggc 3600  
 cttcaaaggt gacactattg agagataagt catataaaag ggtcttttgt ggcgaattgt 3660  
 acaaatactt cgcaaaatcc cttgatcgga cacaataaaa caggtttaat attgttttagc 3720  
 ttttgaacaa acattcatgt ctgaatattt ttgtttcttc ccggttaagg agaaattc 3778  
 atg gac cat aag gac ctc gcg caa cgc atc ctg cgc gac att ggc ggc 3826  
 Met Asp His Lys Asp Leu Ala Gln Arg Ile Leu Arg Asp Ile Gly Gly  
 1 5 10 15  
 gaa gac aac att gtc gcc gcc gca cac tgt gca acg cgt tta cgc ctc 3874  
 Glu Asp Asn Ile Val Ala Ala Ala His Cys Ala Thr Arg Leu Arg Leu  
 20 25 30  
 gtg ctc aaa gac acc aag gat gtg gat cgc caa agt ctg gat gat gat 3922  
 Val Leu Lys Asp Thr Lys Asp Val Asp Arg Gln Ser Leu Asp Asp Asp  
 35 40 45  
 cca gat ctg aaa ggc acc ttt gaa act ggc ggc atg ttc cag atc atc 3970

Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile  
50 55 60

gtc ggg cca ggc gat gtg gat cat gtt ttc aaa gaa ctc gat gac gca 4018  
Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala  
65 70 75 80

acc tcc aaa gac atc gct gtg tcc aca gag cag ctc aaa gat gtt gtg 4066  
Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val  
85 90 95

gct aac aac gcc aac tgg ttc agc cgt gct gtg aag gta ttg gcg gac 4114  
Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp  
100 105 110

att ttc gtc ccg ctg att cca atc ttg gtt ggt ggc ggt ctg ctc atg 4162  
Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Gly Leu Leu Met  
115 120 125

gct atc aac aat gtg ttg gtt gcg cag gat ctg ttc ggt ccg caa tca 4210  
Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser  
130 135 140

ctg gtg gag atg ttc cct cag atc agc ggt gtt gct gag atg atc aac 4258  
Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn  
145 150 155 160

ctg atg gca tct gcg ccg ttc gcg ttc ttg cca gtg ttg gtt ggt ttc 4306  
Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe  
165 170 175

acc gca acc aag cgt ttc ggt ggc aat gag ttc ctg ggc gcc ggc att 4354  
Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile  
180 185 190

ggt atg gcg atg gtg ttc cca acc ctg gtt aac ggc tac gac gtg gcc 4402  
Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala  
195 200 205

gcc acc atg acc gcg ggc gaa atg cca atg tgg tcc ctg ttt ggt ttg 4450  
Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu  
210 215 220

gat gtt gct caa gct ggt tac cag ggc acc gtg ctt cct gtg ctg gtg 4498  
Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val  
225 230 235 240

gtc tct tgg att ctg gca acg atc gag aag ttc ctg cac aag cga ctc 4546  
Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu  
245 250 255

atg ggc act gca gac ttc ctg atc acc cca gtg ttg act ctg ctg ctc 4594  
Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu  
260 265 270

acc ggc ttc ctt acg ttc att gct att ggt cca gca atg cgc tgg gtg 4642  
Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val

275	280	285	
ggt gac ttg ctg gca cac ggt ctg cag gga ctc tat gat ttc ggt ggt Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly 290 295 300			4690
cca gtc ggc ggt ctg ctt ttc ggt ctg gtc tac tca cca atc gtt atc Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile 305 310 315 320			4738
act ggt ctg cac cag tcc ttc ccg cca att gag ctg gag ctg ttc aac Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn 325 330 335			4786
cag ggt gga tcc ttc atc ttc gca acc gca tcc atg gcc aat atc gcg Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala 340 345 350			4834
cag ggt gca gca tgt ttg gca gtg ttc ttc cta gcg aag agt gaa aag Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys 355 360 365			4882
ctc aag ggc ctt gca ggt gct tca ggt gtc tcc gct gtt ctt ggt att Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile 370 375 380			4930
aca gag cct gcg atc ttc ggt gtg aac ctt cgc ctg cgc tgg ccg ttc Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe 385 390 395 400			4978
tac att ggt atc ggt acc gca gct atc ggt ggc gct ttg att gca ctc Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu 405 410 415			5026
ttt gat atc aag gca gtt gcg ttg ggc gct gca ggt ttc ttg ggt gtt Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val 420 425 430			5074
gtt tct att gat gct cca gat atg gtc atg ttc ttg gtt tgc gcg gta Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val 435 440 445			5122
gtt acc ttt gtc atc gca ttc ggc gca gcg att gct tat ggc ctt tac Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr 450 455 460			5170
ttg gtt cgc cgc aac ggc agc att gat cca gat gca acc gct gct cca Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro 465 470 475 480			5218
gtg cct gca gga acg acc aaa gcc gaa gca gaa gca ccc gca gaa ttt Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe 485 490 495			5266
tca aac gat tcc acc atc atc cag gca cct ttg acc ggt gaa gct atc Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile 500 505 510			5314

gca ctg agc agc gtc agc gat gcc atg ttt gcc agc gga aag ctt ggc 5362  
Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly  
515 520 525

tca ggt gtt gcg atc gtc ccc acc aag ggg cag ctg gtt tca cca gtg 5410  
Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val  
530 535 540

agc gga aag atc gtg gtg gcc ttc cca tct ggt cac gct ttc gca gtc 5458  
Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val  
545 550 555 560

cgc act aag gct gag gat ggt tcc aat gtg gat atc ttg atg cac att 5506  
Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile  
565 570 575

ggt ttc gac acc gta aac ctc aac ggc acg cac ttt aac ccg ctg aag 5554  
Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys  
580 585 590

aag cag ggc gat gaa gtc aaa gca ggg gag ctg ctg tgt gaa ttc gat 5602  
Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp  
595 600 605

att gat gcc att aag gct gca ggt tat gag gta acc acg ccg att gtt 5650  
Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val  
610 615 620

gtt tcg aat tac aag aaa acc gga cct gta aac act tac ggt ttg ggc 5698  
Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly  
625 630 635 640

gaa att gaa gcg gga gcc aac ctg ctc aac gtc gca aag aaa gaa gcg 5746  
Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala  
645 650 655

gtg cca gca aca cca taagttgaaa ccttgagtgt tcgcacacag gttagactag 5801  
Val Pro Ala Thr Pro  
660

gggacgtgac tctacgcatac tttgacaccg gtaccggtac gcttcgagat tttaaacctg 5861

ttcaaccagg tcatgcctcg gtgtacctgt gtggtgccac cccgcaatct tcaccccaca 5921

ttggacatgt tcgttcagca gtagcgtttg atattttgcg ccgctgaa 5969

<210> 2  
<211> 661  
<212> PRT  
<213> Brevibacterium lactofermentum

<400> 2

Met Asp His Lys Asp Leu Ala Gln Arg Ile Leu Arg Asp Ile Gly Gly  
1 5 10 15

Glu Asp Asn Ile Val Ala Ala Ala His Cys Ala Thr Arg Leu Arg Leu  
 20 25 30

Val Leu Lys Asp Thr Lys Asp Val Asp Arg Gln Ser Leu Asp Asp Asp  
 35 40 45

Pro Asp Leu Lys Gly Thr Phe Glu Thr Gly Gly Met Phe Gln Ile Ile  
 50 55 60

Val Gly Pro Gly Asp Val Asp His Val Phe Lys Glu Leu Asp Asp Ala  
 65 70 75 80

Thr Ser Lys Asp Ile Ala Val Ser Thr Glu Gln Leu Lys Asp Val Val  
 85 90 95

Ala Asn Asn Ala Asn Trp Phe Ser Arg Ala Val Lys Val Leu Ala Asp  
 100 105 110

Ile Phe Val Pro Leu Ile Pro Ile Leu Val Gly Gly Gly Leu Leu Met  
 115 120 125

Ala Ile Asn Asn Val Leu Val Ala Gln Asp Leu Phe Gly Pro Gln Ser  
 130 135 140

Leu Val Glu Met Phe Pro Gln Ile Ser Gly Val Ala Glu Met Ile Asn  
 145 150 155 160

Leu Met Ala Ser Ala Pro Phe Ala Phe Leu Pro Val Leu Val Gly Phe  
 165 170 175

Thr Ala Thr Lys Arg Phe Gly Gly Asn Glu Phe Leu Gly Ala Gly Ile  
 180 185 190

Gly Met Ala Met Val Phe Pro Thr Leu Val Asn Gly Tyr Asp Val Ala  
 195 200 205

Ala Thr Met Thr Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu  
 210 215 220

Asp Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val  
 225 230 235 240

Val Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu  
 245 250 255

Met Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu  
 260 265 270

Thr Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val  
 275 280 285

Gly Asp Leu Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly  
 290 295 300

Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile  
 305 310 315 320

Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn  
 325 330 335

Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala  
 340 345 350

Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys  
 355 360 365

Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile  
 370 375 380

Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe  
 385 390 395 400

Tyr Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu  
 405 410 415

Phe Asp Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val  
 420 425 430

Val Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val  
 435 440 445

Val Thr Phe Val Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr  
 450 455 460



Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro  
 465 470 475 480

Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe  
 485 490 495

Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile  
 500 505 510

Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly  
 515 520 525

Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val  
 530 535 540

Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val  
 545 550 555 560

Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile  
 565 570 575

Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys  
 580 585 590

Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp  
 595 600 605

Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val  
 610 615 620

Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly  
 625 630 635 640

Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala  
 645 650 655

Val Pro Ala Thr Pro  
 660

<210> 3  
 <211> 44  
 <212> DNA  
 <213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC DNA

<400> 3

gtacatattg tcgttagaac gcgtaatacg actcactata gggga

44

<210> 4

<211> 47

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC DNA

<400> 4

gtacatattg tcgttagaac gcgtaatacg actcactata gggagag

47

<210> 5

<211> 46

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC DNA

<400> 5

gtacatattg tcgttagaac gcgtaatacg actcactata gggaga

46

<210> 6

<211> 51

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC DNA

<400> 6

gtacatattg tcgttagaac gcgtaatacg actcactata gggagactgc a

51

<210> 7

<211> 47

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC DNA

<400> 7

gtacatattg tcgttagaac gcgtaatacg actcactata gggagag

47

<210> 8

<211> 47

<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 8  
gtacatattg tcgtagaac gcgtaatacg actcactata gggagat

47

<210> 9  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 9  
cgtcttgcca ggattcagcg agctg

25

<210> 10  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 10  
agctggattt cggccatgaa ttcta

25

<210> 11  
<211> 23  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 11  
gatctgttcg gtccgcaatc act

23

<210> 12  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 12  
cactggtgga gatgttcct cagat

25

<210> 13  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 13  
catcttcgca accgcatcca tggcc

25

<210> 14  
<211> 24  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 14  
cgcgagggt gcagcatgtt tggc

24

<210> 15  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 15  
gggccttgca ggtgcttcag gtgtc

25

<210> 16  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 16  
ccgctgttct tggattaca gagcc

25

<210> 17  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 17  
gcagcgtcag cgatgccatg ttg

25

<210> 18  
<211> 25  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 18  
gcttggtca ggtggtgcga tcgtc

25

<210> 19  
<211> 36  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 19  
gtacatattg tcgttagaac gcggtatac gactca

36

<210> 20  
<211> 35  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 20  
cgtagaacg cgtaatacga ctactatag ggaga

35

<210> 21  
<211> 24  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 21  
cgctactgt gaacgaacat gtcc

24